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Fig. 1A

Restriction map of plasmid ms23

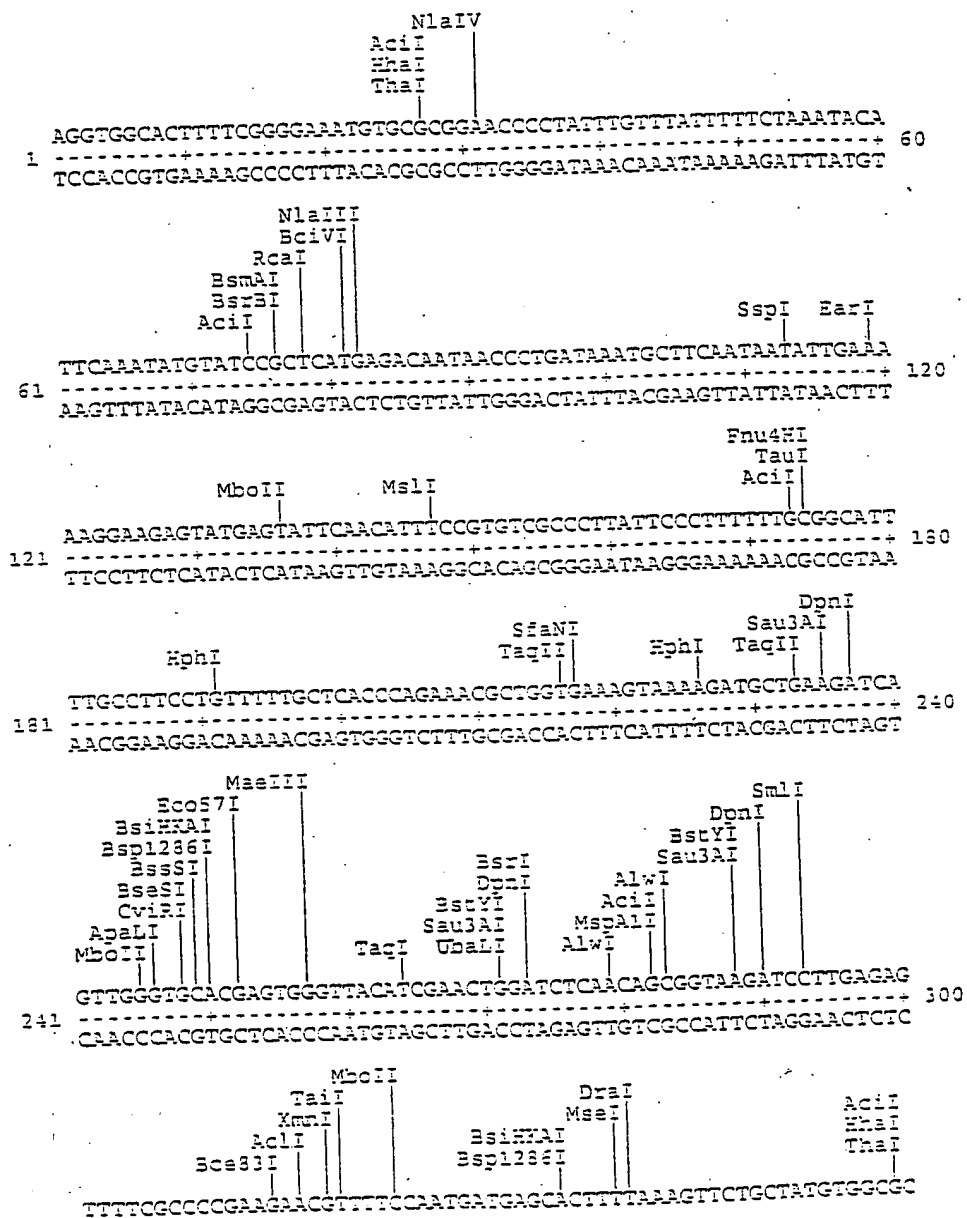
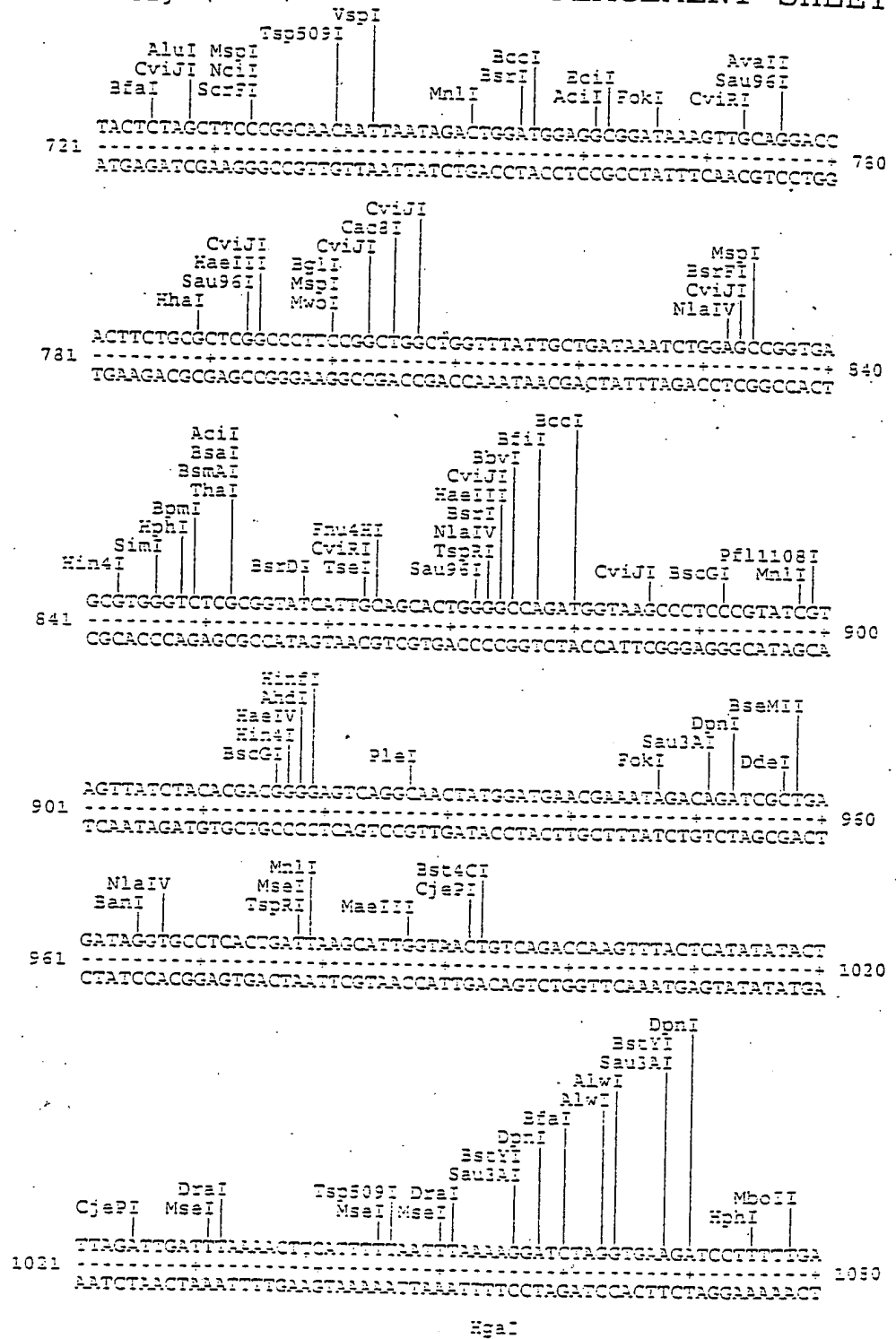


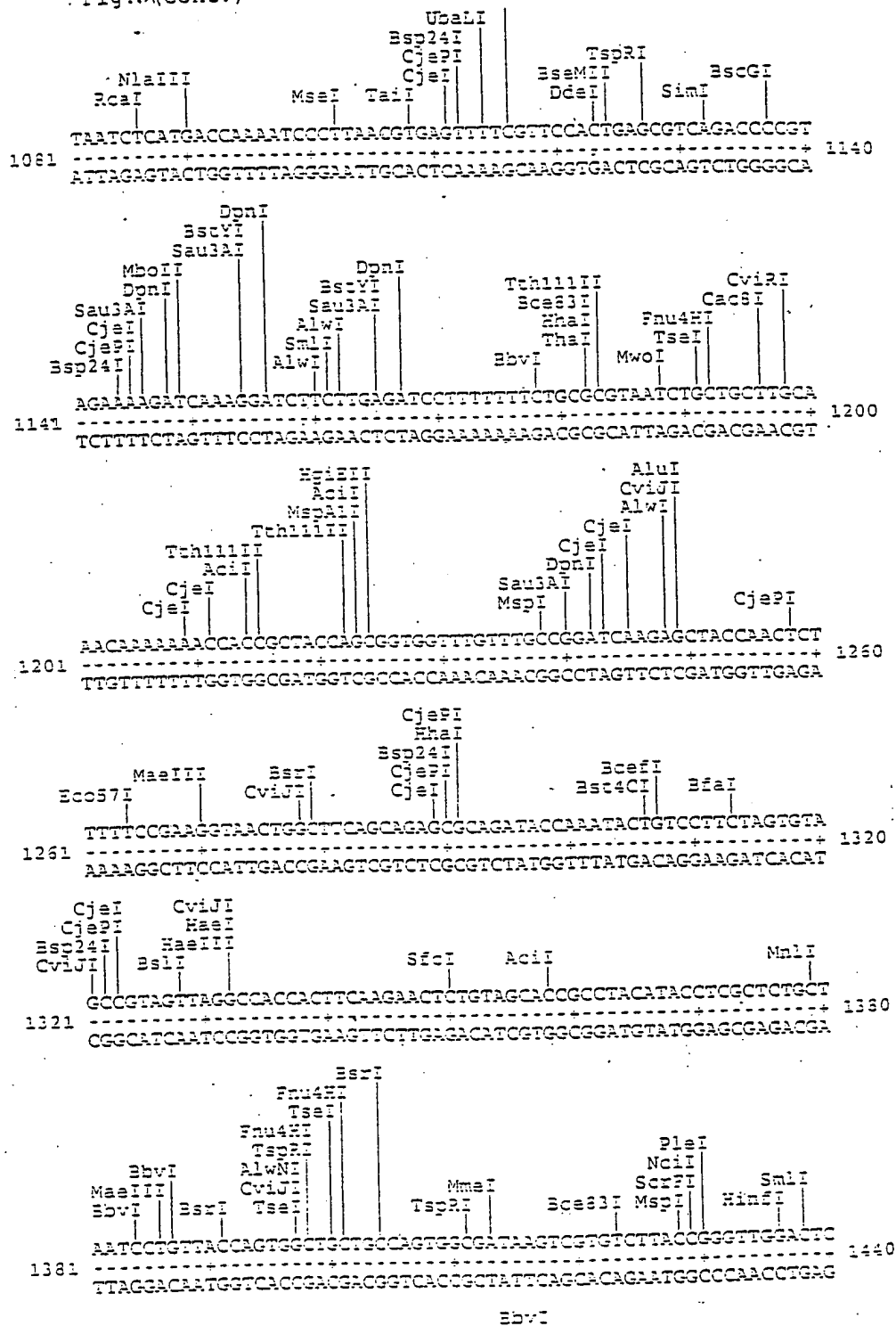
Fig.1A(cont.)

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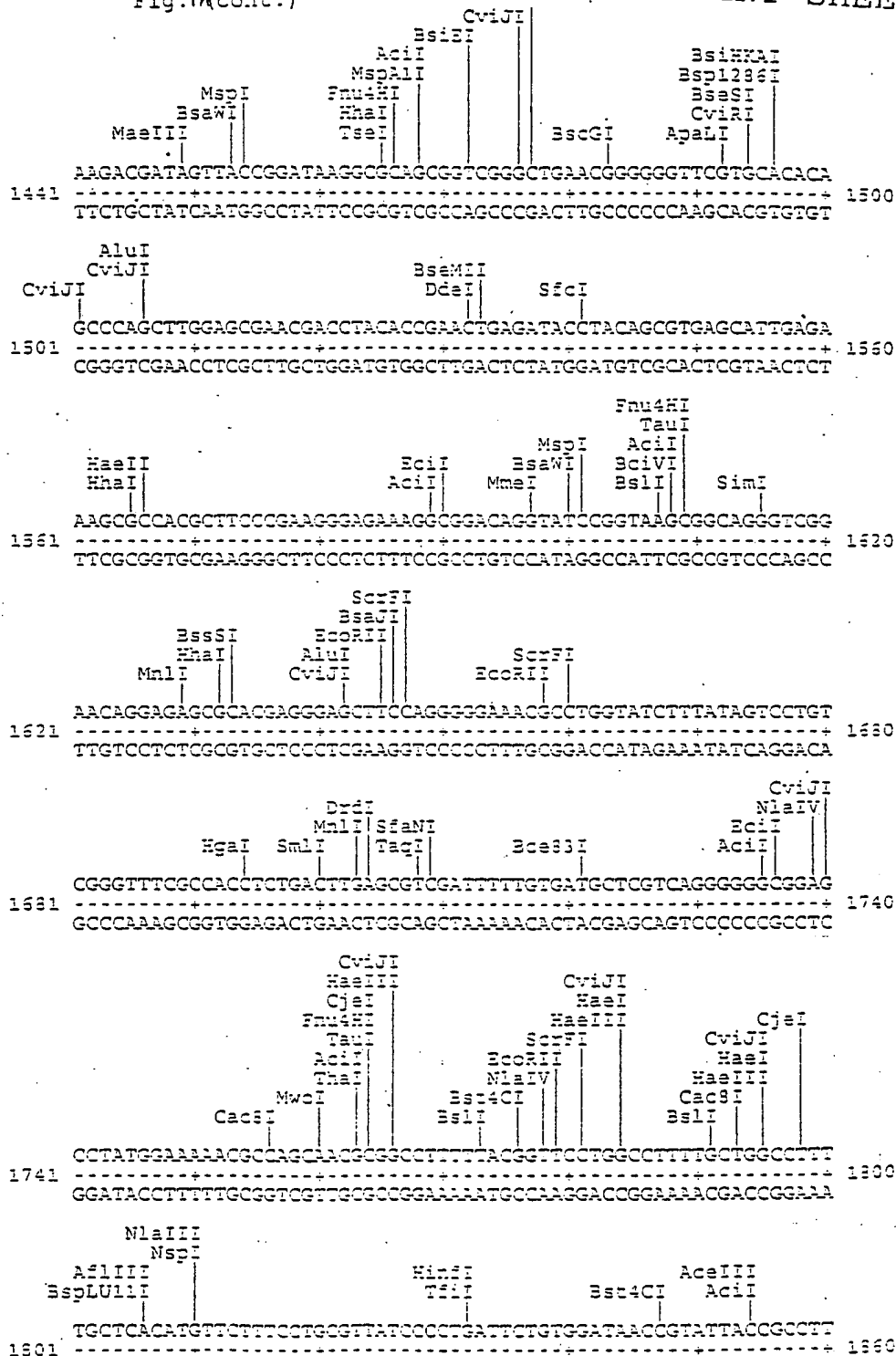
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Fig.1A(cont.)

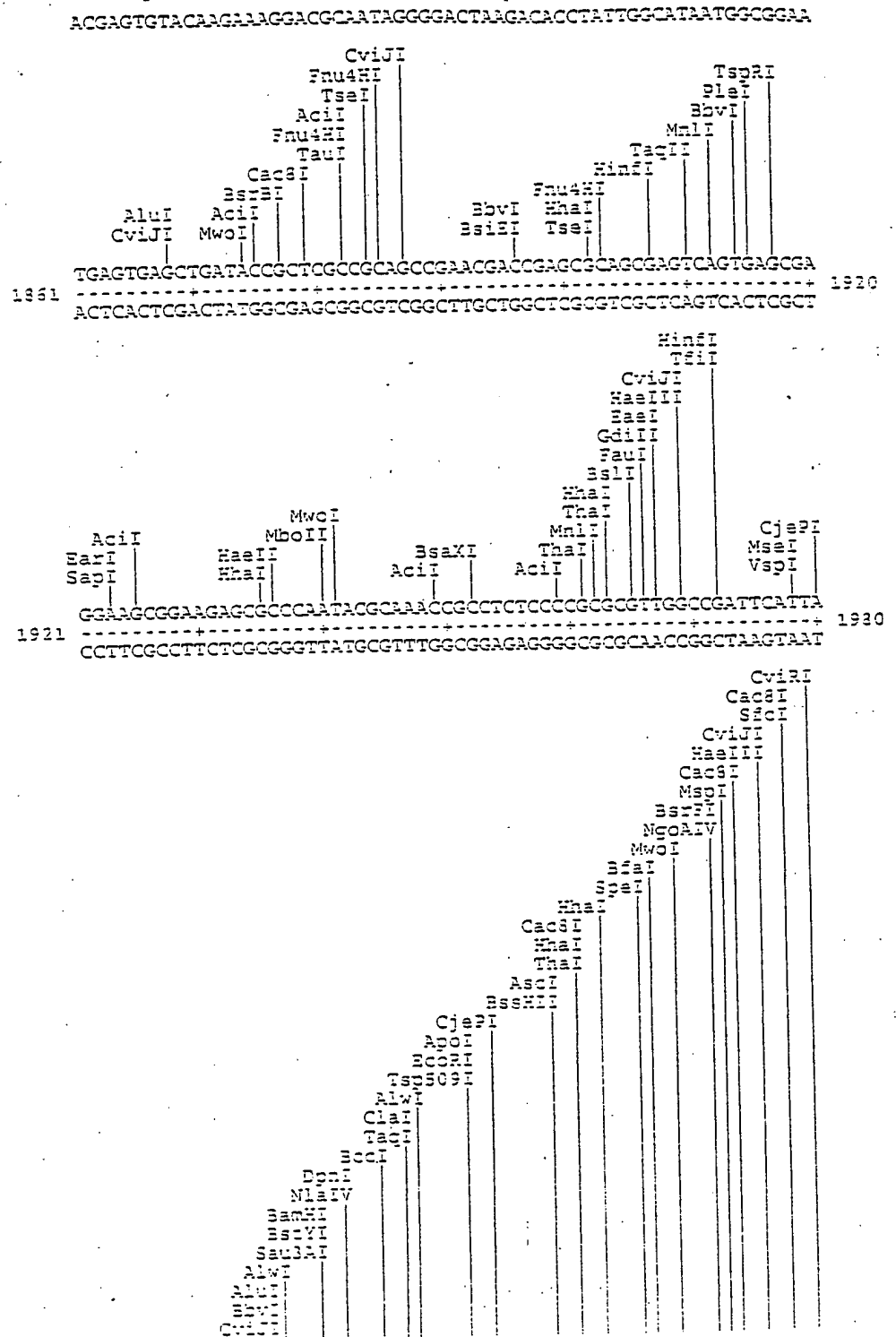


Fig.1A(cont.).

PstI
 BfaI
 XbaI
 HincII
 AccI
 TaqI
 SalI
 BsiII
 AccI
 PstI
 SmaI
 HincII
 MnlI
 MnlI

AGTCTAGAGTCGACCGCAAGACCCCTTCTCTATATAAGGAAGTTTCATTTCATTGGAGAG
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 TCAGATCTCAGCTGGCGTCTCTGGGAAGGAGATATATTCCTTCAGTAAAGTAAACCTCTC

20+1 2100

[illegible]

Restriction sites:

TaqI CviII
EcoRI HaeIII

BamHI

SacII

ClaI

XbaI

KpnI

PstI

HindIII

NheI

AlwI

EcoRV

TspXI

SmaI

BclII

DpnI

AACTCGACGGCCTGTGCGATTTCATCTCTGGATTCGCGAAGACTGTGGCAATTCATCATCGTT

Fig.1A(cont.:)

2161 TTTGAGCTGCCGGACACCCGTAAGTCAGACCTAGCGCTTTTGACACCTTAACTAGTCGCAA 2220

MunI
Tsp509I
CjaPI
MaeIII
KhaI
ThaI
NciI
ScrFI
MspI
CviJI
SmaI
ScaI
SmaI
DpnI
SfaNI

2221 GGTGGGAAAGCGCGTTACAAGAAAGCCGGGCAATTGCTGTGCCAGGCAGTTTAAACGATC 2230

CCACCCCTTTTCGCGCAATGTTCTTTTCGGGCCGTTAACGACACGGTCCGTCGAATTTGCTAG

FauI
Cac8I
AcII
Tsp509I
CviRI
Tsp45I
KhaI
ThaI
TaqI
RseI

2281 AGTTCCGCGATGCAGATATTTCGTAATTATGCGGGCAACGTCCTGGTATCAGCGCGAAGTCT 2340

TCAAGCGGCTACGTCCTATAAGCATTAAATACGCCCGTTGCAGACCATAGTCGCGCTTCAGA

Cac8I
BbvI
CviJI
HaeI
HaeIII
Cac8I
Fnu4HI
SfaNI
TseI
MwoI
MaeIII
Tsp45I
AcII
RseI

2341 TTATACCGAAAGGTTGGGCAGGCCAGCGTATCGTGCTGCGTTTTGCGATGCGGTCAGTCATT 2400

AATATGGCTTTTCCAACCCGTCGCGTCGCATAGCAGCAGCGCAAGCTACGCCAGTCAGTAA

CviJI
Fnu4HI
SfaNI
Tsp45I
HaeIV
Hin4I
BccI
BceII
SmaI
SimI

2401 ACGGCARAGTGTGGGTCAATATCAGGAATGATGGAGCATCAGGGCGGCTATACGCCAT 2460

TGCCGTTTCACACCCAGTTATTAGTCCTTCACTACCTCGTAGTCCCGCCGATATGCGGTA

MaeIII
Tsp45I
CviJI
BceII
NciI
ScrFI
MspI
HphI
Bst4CI
CjaPI
TaqI
EsaI
SnaBI
RsaI

2461 TTGAAGCCGATGTCACGCCGATGTTATTGCGGGGAAAGTGATCGTATCACCCTTTGTG 2520

AACCTTCGGCTACAGTGCGGCATACAATAACGGCCCTTTTCACATGCATAGTGGCAACAC

FauI
NciI
ScrFI
CjaPI
MspI
BstI
AcII
HphI

2521 TGAACAACGAAGTGAAGTGGCAGACTATCCCGCCGGGAATGGTGATTACCGACGAAACG 2580

ACTTGCTTGCTTGACTTGACCGTCTGATAGGGCGGCCCTTACCCTAATGGCTGCTTTTGC

HinFI
Tsp45I
Fnu4HI
TseI
BccI
MspI
MaeI
NlaIII
BceII

2561 GCAAGAAAAAGCAGTCTTATTTCCATGATTTCTTTAACTATGCGGGAATCCATCGCAGCG 2640

CGTTCTTTTTCTGTCAGAATGAAGTACTAAAGAAATTTGATACGGCCCTTAGGTAGCGTCCG

Fig.1A(cont.)

Fig. 1A (cont.)

MaeIII
Tsp45I
HgaI
NheI
MwoI
NlaIII
NspI
PshAI
Bst4CI
BsaJI
BstDSI
EcoRV
KphI
EcoRII
SbfI
MslII
BbvI
TaqII

2541 TAATGCTCTACACCACGCCGAACACCTGGGTGGACGATATCACCCTGGTGACGCATGTCC

ATTACCGAGATGTGGTGGCGCTTGTGGACCCACCTGCTATAGTGGCACCACTGCGGTACAGC 2700

CviJI
HaeI
HaeIII
MscI
AarI
BsrI
BaeI
HhaI
HgaI
MaeIII
AflIII
MluI
ThaI
HincII
BspMI
DpnI
Sau3AI
BsaBI
AciII
AlwI
CviRI
BspGI
FauI
BfaI
AclI
HphI

2701 CGCAAGACTGTAACCACGCGTCTGTGACTGGCAGGTGGTGGCCAATGGTGATGTTCAGCG

GCGTTCTGACATTGGTGGCGCAGACAACCTGACCGTCCACCACCGGTTACCACTACAGTCCG 2760

SfiNI
DpnI
Sau3AI
BsaBI
AciII
AlwI
CviRI
BspGI
FauI
BfaI
AclI
HphI

2761 TTGAAGTGGTGATGCGGATCAACAGGTGGTGGCACTGGACAAGGCACTAGCGGGACTT

AACTTGACGCACTACGCCTAGTTGTCCACCAACGTTGACCTGTTCCGTTGATCGCCCTGAA 2820

HinfI
TfiI
AciII
HphI
MwoI
NciI
ScrFI
MnlI
MspI
BsiI
HgaI
HphI
Bst4CI
MaeIII
Tsp45I

2821 TGCAAGTGGTGAATCCGCACCTCTGGCAACCGGGTGAAGGTTATCTCTATGAAGTGTGCG

ACGTTCAACCACTTAGCGCTGGAGACCGTTGGCCCCTTCCAATAGAGATACTTGACACGC 2880

CviRI
BsmFI
AciII
HphI
MwoI
NciI
ScrFI
MnlI
MspI
BsiI
HgaI
HphI
Bst4CI
MaeIII
Tsp45I

2881 TCACAGCCAAAAGCCAGACAGAGTGTGATATCTACCCGCTTCGCGTCGGCATCCGGTCAG

AGTGTCCGTTTTTCGGTCTGTCTCACTATAGATGGGCGAAGCGCAGCCGTAGGCCAGTC 2940

BtsI
TspRI
TspRI
Bst4CI
AlwNI
CjaI
MseI
CjaI
Bst4CI
CjaI
BsrI
CviJI
CjaI
BsrI
CviJI

2941 TGGCAGTGAAGGGCGAACAGTTCCTGATTAACCAACAACCGTTCTACTTTACTGGCTTIG

ACCGTCACTTCCCCGTTGTCTAGGACTAATTGGTGTGGCGAAGATGAANTGACCGAAGC 3000

SfiNI
RcaI
NlaIII
MslII
BcgI
AclI
CjaI
AlwNI
CjaI
MseI
CjaI
Bst4CI
CjaI
BsrI
CviJI
CjaI
BsrI
CviJI
ApdLI
MwoI
BccI
BcgI
TaqI
HinfI
TfiI
TaqI
BtaI
BcgI
BsiHYAI
Esp1236I
BseSI
CviRI

3001 GTCGTCATGAAGATGCGGACTTGGCTGGCAAAGGATTGGATACGTTGCTGATGTGACAG

CAGCAGTACTTCTACCGCTGAACGCACCGTTTCTTAAGCTATTGCAAGACTACCAAGTGC 3060

Fig.1A(cont.)

3061
ACCACGCATTAAATGGACTGGATTGGGGCCAACTCCTACCGTACCTCGCATTACCGTTACG
TGGTGCCTAATTACCTGACCTAACCCCGTTGAGGATGGATGAGGCGTAATGGGAATGC

3120

3121
CTGAGGAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAACCTGCTG
GACTTCTCTACGAGCTGACCCGCTCTACTTGTACCGTAGCACCCTAACTACTTTGACGAC

3180

3181
CTGTCGGCTTTAACCTCTCTTTAGGCATTGGTTTCGAAGCGGGCAACAAGCCGAAAGAAC
GACAGCCGAAATGGAGAGAAATCCGTAACCAAGCTTCGCCCGTTGTTCCGCTTTCTTG

3240

3241
TGTACAGCGAAGAGGCAGTCAACGGGGAACCTCAGCAAGCGCACTTACAGGCGATTAAAG
ACATGTGCCTTCTCCGTCACTTGCCTTCTGAGTCGTTCCGCGTAATGTCCGCTAATTTC

3300

3301
AGCTGATAGCGCGTGACAAAAACCAAGCGTGGTGATGTGGAGTATTGCCAACGAAC
TCGACTATCGCGCACTGTTTTGGTGGGTTCCGACCACTACACCTCATACGCTTGCCTG

3360

3361
CGGATACCCGTCGCGAAGGTGCACGGGAATATTTCCGCGCACTGGCGGAGCAACGCGTA
GCCTATGGGCGAGCGCTTCCAGCTGCCCTTATAAAGCGCGGTGACCGCCTTCGTTGCGCAT

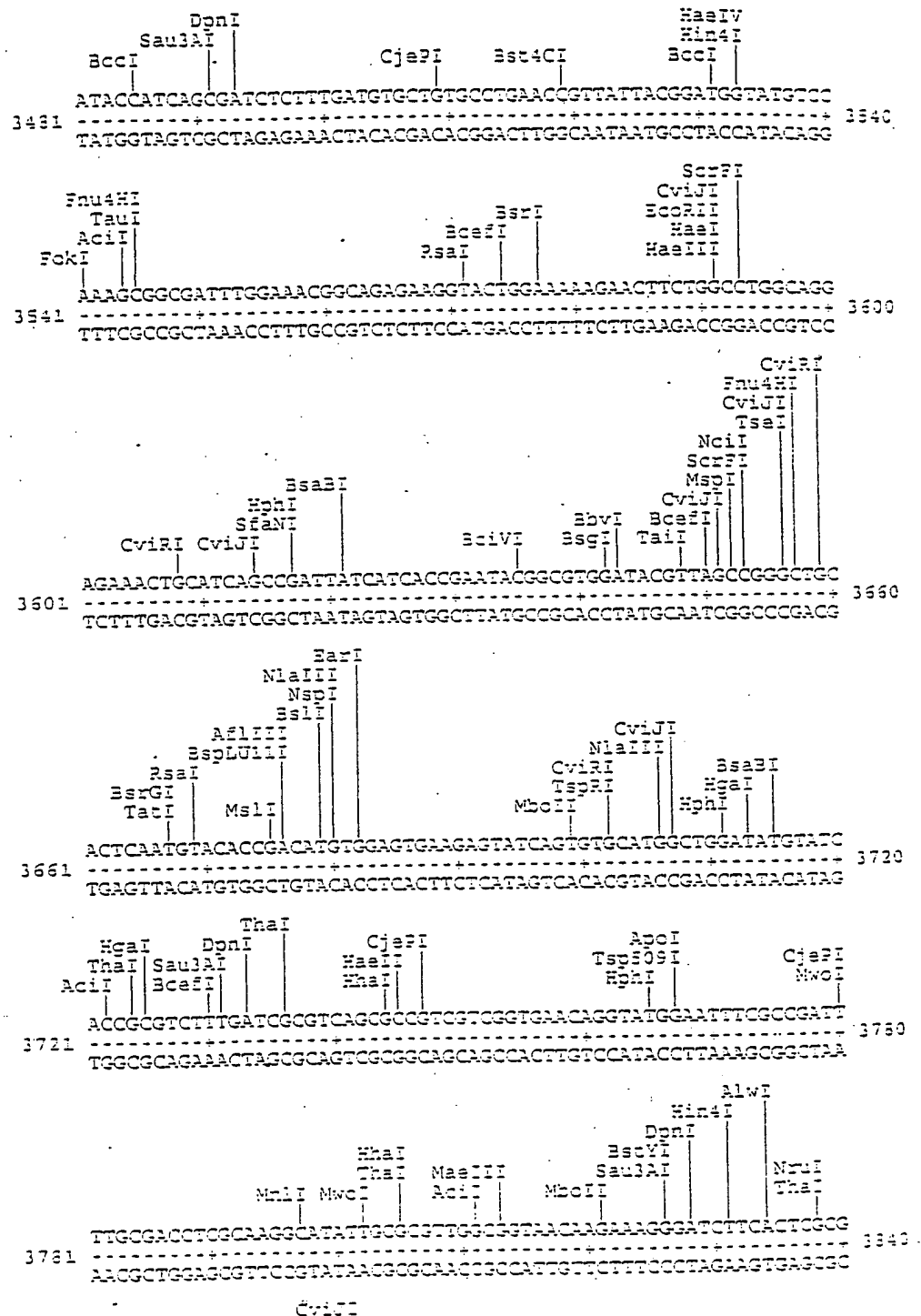
3420

3421
AACTCGACCGGAGCGCTTCGATACCTGCGTCAATGTAATGTTGTGCGAGCGTCAACCG

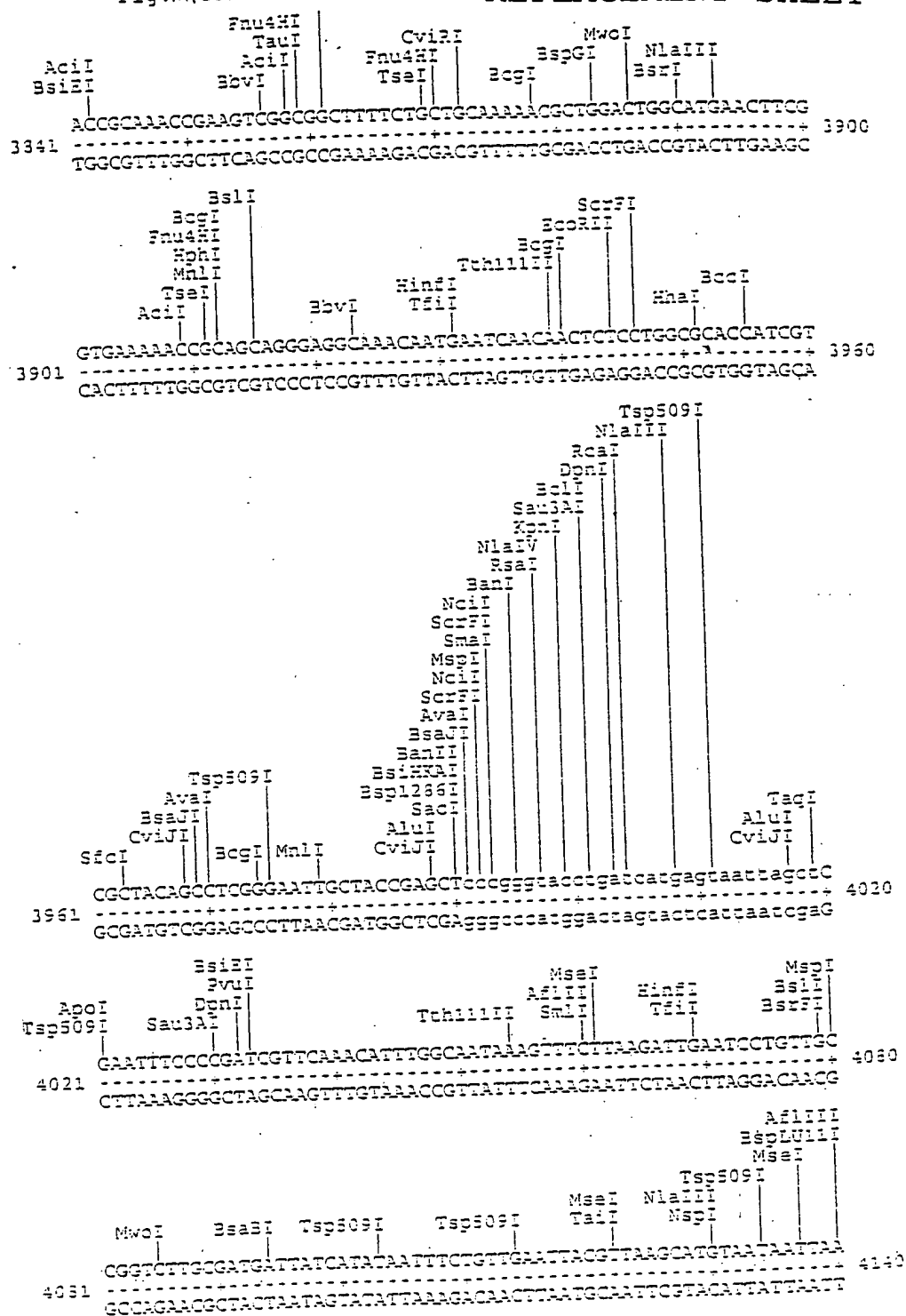
3480

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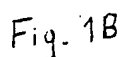
TTGAGCTGGGCTGCCAGGCTAGTCGACGCAGTTACATTACAGACGCTGCGAGTGTGGC



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[illegible]

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pGPTV-GUS-kan

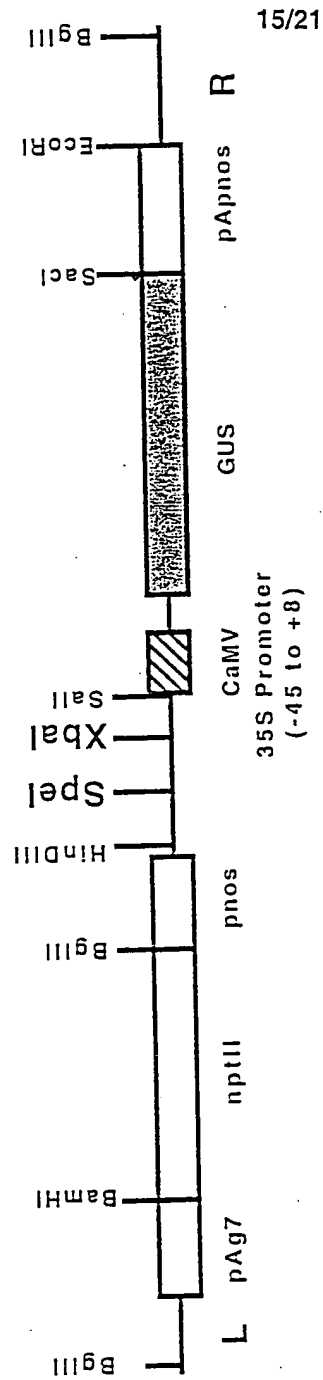


Fig. 3

Fig. 4

